

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-31 (Cancelled).

32. (Original) A method for producing a genetic map for a species, said method comprising:
- a) determining a pattern of hybridization products on an array for sets of samples, wherein each sample within a set contains a different collection of fractionated genomic nucleic acid from a member of said species, wherein said member is different for each set, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within the genome of said species, wherein said hybridization products are formed between said nucleic acid molecules and said fractionated genomic nucleic acid, and
  - b) determining the relationship between said nucleic acid sequences within said genome based on the pattern of hybridization products for each sample of each set and the genetic relationship of said different members for each set, thereby forming said genetic map.
33. (Original) The method of claim 32, wherein said species is a plant species.
34. (Original) The method of claim 32, wherein said species is maize.
35. (Original) The method of claim 32, wherein said sets comprise at least five sets.
36. (Original) The method of claim 32, wherein said sets comprise at least ten sets.

37. (Original) The method of claim 32, wherein each set comprises at least five samples.
38. (Original) The method of claim 32, wherein each set comprises at least ten samples.
39. (Original) The method of claim 32, wherein said genomic nucleic acid was digested with at least two restriction enzymes.
40. (Original) The method of claim 32, wherein said genomic nucleic acid was digested with at least five restriction enzymes.
41. (Original) The method of claim 32, wherein said fractionated genomic nucleic acid is labeled.
42. (Original) The method of claim 32, wherein each nucleic acid molecule is unique.
43. (Original) The method of claim 32, wherein said array comprises at least about 100 nucleic acid molecules.
44. (Original) The method of claim 32, wherein said array comprises at least about 500 nucleic acid molecules.
45. (Original) The method of claim 32, wherein said array comprises at least about 1000 nucleic acid molecules.
46. (Original) The method of claim 32, wherein every twenty-five cM region of said genome contains at least one of said nucleic acid sequences.

47. (Original) The method of claim 32, wherein every two cM region of said genome contains at least one of said nucleic acid sequences.

48. (Original) The method of claim 32, wherein said determining the relationship between said nucleic acid sequences within said genome is determining the relative position of said nucleic acid sequences within said genome.

49. (Original) The method of claim 32, wherein said determining the relationship between said nucleic acid sequences within said genome is determining the relative distance between said nucleic acid sequences within said genome.

50. (Original) A method of producing a genetic map for a species, said method comprising contacting an array with sets of samples, wherein each sample within a set contains a different collection of fractionated genomic nucleic acid from at least one member of said species, said member(s) being different for each set, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within the genome of said species, said contacting being performed such that a pattern of hybridization products is formed for each sample of each set, said hybridization products being formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein the relationship between said nucleic acid sequences within said genome is determinable based on the pattern of hybridization products for each sample of each set and the genetic relationship of said different members for each set, said relationship being said genetic map.

Claims 51-54 (Cancelled).

55. (Original) A method of genotyping a member of a species, said method comprising determining a pattern of hybridization products on an array for a plurality of samples, wherein

each sample contains a different collection of fractionated genomic nucleic acid from said member, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence corresponding to a different sequence within the genome of said species, wherein said hybridization products are formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein said pattern indicates the genotype of said member.

Claims 56-95 (Cancelled).